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FastDB - Fast Pairwise Comparison of Sequences  
Release 5.4

Results file us-09-746-783-18-inv.res made by bobryen on Tue Jun 18 Jun 102 14:36:31-PDT.

Query sequence being compared: US-09-746-783-18' (1-481)  
Number of sequences searched: 154  
Number of scores above cutoff: 134

Results of the initial comparison of US-09-746-783-18' (1-481) with:  
File : US08958304.seq  
File : US09092722.seq  
File : US09096287.seq  
File : US09098588.seq  
File : US09130189.seq  
File : US09149633.seq  
File : US09165960A.seq  
File : US09185936.seq

100-  
N -  
U - 50-  
M -  
B -  
E -  
R -  
O -  
F - 10-  
S -  
E - 5-  
Q -  
U -  
E -  
N -  
C -  
S -  
SCORE 0 12 23 35 47 58 70 82 93 105  
SIDEV 0 0 1 1 2 2 3 4 4 4

Similarity matrix  
Mismatch penalty 1  
Gap penalty 5.00  
Gap size penalty 0.33  
Cutoff score 1  
Randomization group 0

## SEARCH STATISTICS

Scores: Mean 26 Median 22 Standard Deviation 19.60  
Times: CPU 00:00:00.04 Total Elapsed 00:00:01.00

Number of residues: 126429  
Number of sequences searched: 154  
Number of scores above cutoff: 134

The scores below are sorted by initial score.

Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Score	Init. Opt. Frame	Sig.
1. US-09-130-189-7 Sequence 7, Application US	**** 4 standard deviations above mean ****	1865	105	184	0
2. US-08-958-304-12 Sequence 12, Application	**** 2 standard deviations above mean ****	533	69	154	0
3. US-09-098-588-19 Sequence 19, Application		3109	69	168	2.19
4. US-09-165-960-11 Sequence 11, Application		883	68	162	2.14
5. US-08-958-304-3 Sequence 3, Application US		2859	67	175	2.09
6. US-09-149-633-3 Sequence 3, Application US	**** 1 standard deviation above mean ****	947	63	170	0
7. US-09-130-189-13 Sequence 13, Application		4337	62	169	1.89
8. US-09-185-936-3 Sequence 3, Application US		1276	60	164	1.73
9. US-09-165-960-5 Sequence 5, Application US		1573	60	168	1.73
10. US-08-958-304-14 Sequence 14, Application		458	57	172	1.58
11. US-09-098-287-1 Sequence 1, Application US		2636	57	177	1.58
12. US-09-098-588-9 Sequence 9, Application US		951	54	177	1.43
13. US-09-130-189-3 Sequence 3, Application US		1425	54	178	1.43
14. US-09-165-960-9 Sequence 9, Application US		510	53	167	1.38
15. US-09-149-633-7 Sequence 7, Application US		2487	53	124	1.38
16. US-09-185-936-5 Sequence 5, Application US		1108	52	149	1.33
17. US-08-958-304-19 Sequence 19, Application		1257	52	177	1.33
18. US-08-958-304-7 Sequence 7, Application US		2956	51	91	1.28
19. US-09-092-722-18 Sequence 18, Application		1598	50	172	1.22
20. US-08-958-304-17 Sequence 17, Application		481	50	153	1.22
21. US-09-092-722-11 Sequence 11, Application		2043	50	155	1.22
22. US-09-165-960-3 Sequence 3, Application US		1422	49	170	1.17
23. US-09-130-189-9 Sequence 9, Application US		2094	49	179	1.17
24. US-09-092-722-12 Sequence 12, Application		2343	49	175	1.17
25. US-09-092-722-17 Sequence 17, Application		505	48	150	1.12
26. US-09-098-588-5 Sequence 5, Application US		1010	48	151	1.12
27. US-09-130-189-5 Sequence 5, Application US		1921	48	158	1.12
28. US-09-096-287-9 Sequence 9, Application US		2773	48	164	1.12
29. US-09-092-722-14 Sequence 14, Application		324	47	103	1.07
30. US-09-092-722-5 Sequence 5, Application US	**** 0 standard deviation from mean ****	894	45	181	0
31. US-09-092-722-10 Sequence 10, Application		939	45	156	0.97
32. US-09-130-189-15 Sequence 15, Application		1299	45	163	0.97
33. US-09-130-189-17 Sequence 17, Application		791	44	150	0.92
34. US-09-098-588-15 Sequence 15, Application		1240	44	170	0.92
35. US-09-130-189-11 Sequence 11, Application		2069	44	167	0.92
36. US-09-098-588-13 Sequence 13, Application		722	43	140	0.87
37. US-09-149-633-5 Sequence 5, Application US		1335	43	166	0.87
38. US-09-092-722-7 Sequence 7, Application US		2120	42	79	0.82
39. US-08-958-304-21 Sequence 21, Application		1544	41	159	0.77
40. US-09-096-287-15 Sequence 15, Application		1694	39	148	0.66
41. US-09-098-588-1 Sequence 1, Application US		1748	39	165	0.66
42. US-09-130-189-19 Sequence 19, Application		2012	39	163	0.66
43. US-08-958-304-11 Sequence 11, Application		225	38	73	0.61
44. US-09-092-722-3 Sequence 3, Application US		1263	38	159	0.61

1. US-09-746-783-18' (1-481)  
US-09-130-189-7 Sequence 7, Application US/09130189

Initial Score = 105 Optimized Score = 184 Significance = 4.03  
Residue Identity = 40% Matches = 203 Mismatches = 278  
Gaps = 16 Conservative Substitutions = 0

GCCTTAATGAGAGACCCAGCTTTCTTTCTTTGTTGTTATGTTTAAAGCCCTCTGCTGTTTCACGTA  
20 30 40 50 60 70 80





TACACCAGGGAAGTGCATG-----AAAATCCCGTGTTAGTTGGATCACGTAGCTGTCTCCTTAATT  
| | | | |  
CTATGTTGCCTTTGATGATGGTCAGAAAGGCTCAAGCAGTCTGCTCTCAGATGATAAAGGACGCTTGTGTG

	10	20	30	40	50
Initial Score	60	Optimized Score	168	Significance	1.73
Residue Identity	36%	Matches	179	Mismatches	302
-	8	Conservative Substitutions	-	-	0



ACAAAGCTCAAAAATCAGGTTCGATCGAATCCACTCTATAACAGCAATTATTTCTTGAATCTTGAGA  
 TTTTCCCACAGCCCCCTTAACATTGGTCTCTCATGCATTCACAATACATT-TTCATTTGTTTTCCAAAAA  
 380 390 400 410 420 430 440

Gaps	-	3	Conservative Substitutions	-	0		
		X	10	20	30	40	50
		TTTTTTTTTTTTTTTTTTTT	TTTTTTTTTTTTTTTTTTTT	GCCATTCATGTCACAACT			





CTGGCGGACAAACTGCGACATGGTTCACATTTTCTTCGAAAGCGTGGTCCCTCCACAAAGAGTGTTCGCG	140	150	160	170	180	190	200
220	230	240	250	260	270	280	
TTGAACATCTGAAATGTTGGTATTGTTTGTATGTGACAAAGTTTCACCCAGCTCAGTGAAGAAACAGAAACATC	111	111	111	111	111	111	111
TTTCCCATGAGCGTGGCTTAACCTGGTGCATCATCAAAACAAATACCCACATTTGAGATGTTCCAGAAAGCCAGA	210	220	230	240	250	260	270
290	300	310	320	330	340	350	360
CTTTTGCAGGGGCACACCGCTTTTGCAGAAATTTGAACCACTCCGAGTTTGTGTCCGACACTGTCAAAAT	111	111	111	111	111	111	111
AGCTAACCCATTTCTCAAGATCAAAAGATTAATTTTGTCTTTAAGTGGATTCATGACCAACCTGATTT	280	290	300	310	320	330	340
370	380	390	400	410	420	430	
GT-TTTAATTCATTCGTGCTTTTAATTAATCTTACCATGATTTACACCGGAGACGTGATGAAATATCCCC	111	111	111	111	111	111	111
TTGAGATTTTGGGAGGCCGATGCTTAAAAATTTGGAAGCCAGACTCAAGATTAAATGTAACTGATCTCCAG	350	360	370	380	390	400	410
440	450	460	470	X			
TGTTGTTTAACTGGATGATCATCTAGTGTGCTCTTATTTTATACGATATCC	111	111	111	111	111	111	111
GCAAAATACACTCTTGACATTTGAAAAGCCAAAAAAGAAAAAAAAAAAAAAAAAAAAA	430	440	450	460	470	480	

ACACAGGGAAGT--GCGATGAAATACCCCTGTGTTAGTGGATACGTGAGCTGCTCCATTTATT  
 TGGTGCTTTGCAGTACGTGAGATCACCCCTTCACACTCCAGCCTGGATACAGAAATGAAGATGCTGTCTTAATA  
 1520 1530 1540 1550 1560 1570 1580

480  
 ACAGTATTC | | |  
 AAAAAAAAAA | | |  
 1590 X

20. US-09-746-783-18' (1-481)  
US-08-958-304-17 Sequence 17, Application US/08958304

Initial Score	=	50	Optimized Score	=	172	Significance	=	1.222
Residue Identity	=	39%	Matches	=	194	Mismatches	=	287
Gaps	=	12	Conservative Substitutions	=			=	0

[illegible]

AGAAATGGGTTACCTTCCTGCTTTT	200	210	220	230	240	250
-----CTTGAACATCTGAATAGTGGTATTGTTTGTATGACAACTT						
TGATATGGCTGGGTGTGTGCTTACACCTGTATCCACACAGTTTGGAGCCTGAGTGGGAGATTCCT	1300	1310	1320	1330	1340	1350
					1360	1370

260	270	280	290	300	310	320	330
TCAGCAGCTATGGA	AAACAGGAACAT	CTTTTTCAGGGAC	CACACCGTTTCAG	AGAAATTTGAAC	CT		
TTAGCCCAAGAGTT	GGAGACAGCC	CTGGACAAAT	TGACCTCTCT	CACAAAATTC	AAAAATTTGGCT	GG	
1380	1390	1400	1410	1420	1430	1440	

340 350 360 370 380 390 400  
GGGATTTTGTCCGGGACAGCTGTAAATAATTTTAATTCATGCTGCTTTAATTAATCCTACATGTT  
GTTGTTGGACACAGCTGTGTCCTCCAGCTACCGGAGACGTGAGGTGGAGATTTGCTTACGCCCGGAGAGA  
1450 1460 1470 1480 1490 1500 1510

410 420 430 440 450 460 470

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FastDB - Fast Pairwise Comparison of Sequences  
Release 5.4

Results file us-09-746-783-18.res made by bobryen on Tue Jun 18 102 14:35:57-PDT.

Query sequence being compared: US-09-746-783-18 (1-481)  
Number of sequences searched: 154  
Number of scores above cutoff: 154

Results of the initial comparison of US-09-746-783-18 (1-481) with:

File : US08958304.seq  
File : US09092722.seq  
File : US09066287.seq  
File : US09098588.seq  
File : US09130189.seq  
File : US09149633.seq  
File : US09165960A.seq  
File : US09185936.seq

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F 10-  
S -  
E 5-  
Q -  
U -  
N -  
C -  
S -  
SCORE 0 | 53 | 107 | 160 | 214 | 267 | 321 | 374 | 428 | 481 |  
STDEV 0 | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 |  
PARAMETERS  
Similarity matrix Unitary K-tuple 4  
Mismatch penalty 1 Joining penalty 30  
Gap penalty 5.00 Window size 481  
Gap size penalty 0.33  
Cutoff score 1  
Randomization group 0  
SEARCH STATISTICS  
Scores: Mean Median Standard Deviation  
29 23 41.90  
Times: CPU Total Elapsed  
00:00:00.95 00:00:01.00

Number of residues: 126429  
Number of sequences searched: 154  
Number of scores above cutoff: 154  
The scores below are sorted by initial score.

Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was found:

Sequence Name	Description	Length	Score	Init. Opt. Sig. Frame
1. US-09-092-722-18	Sequence 18, Application	481	481	481 10.79 0

The list of other best scores is:

Sequence Name	Description	Length	Score	Init. Opt. Sig. Frame
2. US-09-096-287-7	Sequence 7, Application US	588	113	194 2.00 0
3. US-09-149-633-7	Sequence 7, Application US	2487	89	189 1.43 0
4. US-09-098-588-3	Sequence 3, Application US	2298	80	193 1.22 0
5. US-08-958-304-9	Sequence 9, Application US	1325	69	185 0.95 0
6. US-08-958-304-19	Sequence 19, Application	1257	68	185 0.93 0
7. US-09-165-960-13	Sequence 13, Application	1110	65	185 0.86 0
8. US-09-185-936-5	Sequence 5, Application US	1108	64	184 0.84 0
9. US-09-165-960-14	Sequence 14, Application	861	61	168 0.76 0
10. US-09-096-287-9	Sequence 9, Application US	2773	59	179 0.72 0
11. US-09-185-936-9	Sequence 9, Application US	1294	58	172 0.69 0
12. US-09-149-633-15	Sequence 15, Application	984	57	175 0.67 0
13. US-09-096-287-17	Sequence 17, Application	1309	55	175 0.62 0
14. US-08-958-304-17	Sequence 17, Application	1598	54	173 0.60 0
15. US-09-098-588-15	Sequence 15, Application	1240	53	189 0.57 0
16. US-09-185-936-3	Sequence 3, Application US	1276	53	187 0.57 0
17. US-08-958-304-3	Sequence 3, Application US	2859	53	173 0.57 0
18. US-09-096-287-15	Sequence 15, Application	1654	52	170 0.55 0
19. US-09-092-722-5	Sequence 5, Application US	884	51	185 0.53 0
20. US-09-149-633-5	Sequence 5, Application US	2120	51	184 0.53 0
21. US-09-165-960-5	Sequence 5, Application US	1573	50	189 0.50 0
22. US-09-130-189-7	Sequence 7, Application US	1865	50	165 0.50 0
23. US-09-092-722-12	Sequence 12, Application	2343	50	173 0.50 0
24. US-09-098-588-13	Sequence 13, Application	722	48	179 0.45 0
25. US-09-185-936-11	Sequence 11, Application	1354	48	167 0.45 0
26. US-09-149-633-11	Sequence 11, Application	1398	48	168 0.45 0
27. US-09-096-287-13	Sequence 13, Application	1592	47	168 0.43 0
28. US-09-130-189-11	Sequence 11, Application	2069	47	178 0.43 0
29. US-09-096-287-19	Sequence 19, Application	1740	46	157 0.41 0
30. US-09-185-936-1	Sequence 1, Application US	2556	46	157 0.41 0
31. US-08-165-960-11	Sequence 11, Application	883	45	171 0.38 0
32. US-09-130-189-9	Sequence 9, Application US	2034	45	183 0.38 0
33. US-09-149-633-13	Sequence 13, Application	2132	45	172 0.38 0
34. US-09-092-722-9	Sequence 9, Application US	75	43	47 0.33 0
35. US-09-130-189-17	Sequence 17, Application	791	42	185 0.31 0
36. US-09-092-722-3	Sequence 3, Application US	1263	42	177 0.31 0
37. US-09-130-189-3	Sequence 3, Application US	1425	42	180 0.31 0
38. US-09-149-633-9	Sequence 9, Application US	3495	42	186 0.31 0
39. US-08-958-304-5	Sequence 5, Application US	933	41	174 0.29 0
40. US-09-185-936-17	Sequence 17, Application	1056	41	171 0.29 0
41. US-09-165-960-9	Sequence 9, Application US	510	40	171 0.26 0
42. US-09-165-960-3	Sequence 3, Application US	1472	40	173 0.26 0
43. US-09-130-189-1	Sequence 1, Application US	2271	40	169 0.26 0
44. US-09-185-936-7	Sequence 7, Application US	2952	39	156 0.24 0
45. US-08-958-304-12	Sequence 12, Application	533	38	154 0.21 0

1. US-09-746-783-18 (1-481)  
US-09-092-722-18 Sequence 18, Application US/09092722

Initial Score = 481 Optimized Score = 481 Significance = 10.79  
Residue Identity = 100% Matches = 481 Mismatches = 0  
Gaps = 0 Conservative Substitutions = 0

X 10 20 30 40 50 60 70  
GGATCTGTAATTAATGAGACAGCTACAGTCCAGCTAAACCAACAGGGGATTTTCATCAGACCTCC  
|||||

GGAACTACTGTAATTAATAGAGACAGACTACAGTACAGTATCCCACTTAACCAACAGAGGGATTTTTCATCAGACCTTTT	10	20	30	40	50	60	70
X	80	90	100	110	120	130	140
CTGGTGTATATCATGGTACAGATATATTTAAAGACACGATGATTTTAAACATTTTGTACACGCTCCGGACACACA	150	160	170	180	190	200	210
CTGGTGTATATCATGGTACAGATATTTTAAAGACACGATGATTTTAAACATTTTGTACACGCTCCGGACACACA	220	230	240	250	260	270	280
AACTGCACAGTGGTTCATTAATTTTCTTGAAAGCGGTGTGTCTCCCTGCAAAGAGATGTTCCTGTATTTCATGAGCC	290	300	310	320	330	340	350
AACTGCACAGTGGTTCATTAATTTTCTTGAAAGCGGTGTGTCTCCCTGCAAAGAGATGTTCCTGTATTTCATGAGCC	360	370	380	390	400	410	420
150	160	170	180	190	200	210	220
220	230	240	250	260	270	280	290
TGGCTGTAAACCTTGTGTACATCAATTAACCAACATACCACATTTTCAGATGTTCAGAAAGACGACGAGATACCTATAT	300	310	320	330	340	350	360
TGGCTGTAAACCTTGTGTACATCAATTAACCAACATACCACATTTTCAGATGTTCAGAAAGACGAGATACCTATAT	370	380	390	400	410	420	430
220	230	240	250	260	270	280	290
TCTCAGAATCTCAAAAGATATATTGTTCGTATATAGAACTGATTCATGAGCAACCTGATTTTGGAGTTTGTG	300	310	320	330	340	350	360
TCTCAGAATCTCAAAAGATATATTGTTCGTATATAGAACTGATTCATGAGCAACCTGATTTTGGAGTTTGTG	370	380	390	400	410	420	430
290	300	310	320	330	340	350	360
GAGCCGATGCTCTAAAAAATTGGAAAGCCAGACTCAAGAAATTAATGTAAAGCTGATCTTCAGAGCAAAATATCACT	370	380	390	400	410	420	430
GAGCCGATGCTCTAAAAAATTGGAAAGCCAGACTCAAGAAATTAATGTAAAGCTGATCTTCAGAGCAAAATATCACT	440	450	460	470	480	490	500
TGCGCATTTTGAAGAGCGCAA	510	520	530	540	550	560	570
TGCGCATTTTGAAGAGCGCAA	580	590	600	610	620	630	640
440	450	460	470	480	490	500	510
440	450	460	470	480	490	500	510

[illegible][illegible][illegible]

```

      50          60          70          80          90         100        110       120
      X                |   |   |   |   |   |   |   |   |   |   |   |   |
GATCTACTGAATAAATAGGACACCGTCAAGTGTG---ATCCAACTAACCAA
      |   |   |   |   |   |   |   |   |   |   |   |   |   |
ATTACGTATGCAGAAAATTAAGTGAATCACAAGTTCTCTTTCCCAAGACATATTTCATCTGTGTGT
      820      830      840      850      860      870      880      890

```

[illegible]





|||||  
AGTGCCTTCTCCCTTGTCATGAGCCGCCCTTACAGACACAGCCATGACAAACAGGATG  
610 620 630 640 650 660 670  
480  
AAAAAA  
CATTGCTCTGTCCTCCACCCGCG  
680 X 690 700

10. US-09-746-783-18 (1-481)  
US-09-096-287-9 Sequence 9, Application US/09096287

Initial Score = 59 Optimized Score = 179 Significance = 0.72  
Residue Identity = 39% Matches = 194 Mismatches = 287  
Gaps = 6 Conservative Substitutions = 0

X  
GATACGTATATAAATAGAGACAGCTAGTATCCAAACCAACAG  
|||||  
TATCATATTTGATTCACATATATATACCTTCTGGGTACTATTTCTGGGCTCTTGGAG  
2260 2270 X 2280 2290 2300 2310 2320  
60 70 80 90 100 110 120  
GGATTTTCATCAGACACTCCCTGCTATCATGTACAGATTATTAAGACAGATTTAAACATT  
|||||  
GTGGTACCTGTCATGATGCTTAAAGAGAGGCTTTTTCATCCAAAGCTAGTGTGGAGGTGGG  
2330 2340 2350 2360 2370 2380 2390

130 140 150 160 170 180 190  
TTTGACAGCTGCGGACACAAACTCGCAGTGTTCATATTTTCGAAAGCGTGGTCCCTCAAAAGAT  
|||||  
TGGGAGAGGACACTTTTGGATTCTGAAGAATCATATCTGTATATATACATATGAGTGGGAGATGGG  
2400 2410 2420 2430 2440 2450 2460  
200 210 220 230 240 250 260  
GTTT--CCTGTTTTCATGAGCTGCTGAGAACTGTACATCAAAACAAATACCATTTTCAGATGTTCAAG  
|||||  
GGTTGGCAGGGGTGAGGAGGAGGACAAACAGTATGAGGAACAGGACATCTCCAGATGGGAG  
2470 2480 2490 2500 2510 2520 2530

270 280 290 300 310 320 330  
AAAAGCCAG--AAGGTAACTTCTTCAGAAATCAAAAGAAATTTGCTGTATAGAGTGCATCATGA  
|||||  
GTACCTGGGTCGCTGCTCTCTCTGTATGCTGTGGGTTATATACACTATATACACTTCTCTGTGGA  
2540 2550 2560 2570 2580 2590 2600 2610

340 350 360 370 380 390 400  
G--CAACCTGATTTTGTGAGCGGATGCTAATAAATTGGNAGCCAAAGACTCAAGAAATTAATGA  
|||||  
GTTCAATGTCCTGCTGTGAGTCTTGTGTATTTGAGCCTCAGTACACTCAAGAGGCACTTAAAGTGAAG  
2620 2630 2640 2650 2660 2670 2680

410 420 430 440 450 460 470  
AGCTGATCTCCAGGCAAAATACACTTGTGACATTTGAAAAGCAAAAAAAAAAAAAAAAAAAAA  
|||||  
CTGAACCTCTGCAAA  
2690 2700 2710 2720 2730 2740 2750

X  
AAA  
|||  
AAAAAAAAAAAAAAAAAAAA  
2760 2770

11. US-09-746-783-18 (1-481)  
US-09-185-936-9 Sequence 9, Application US/09185936

Initial Score = 58 Optimized Score = 172 Significance = 0.69  
Residue Identity = 41% Matches = 211 Mismatches = 260  
Gaps = 34 Conservative Substitutions = 0

X  
GATATCTATTAATATGAGACAGCTACAGTATCCAACTAAACCAACAGG  
|||||  
AAACACTGTGTCAGGCTCTGGGAGAGTTCAGTATGCTCTTGATTTATATGAAATTTGCCCTC  
780 790 800 810 820 830 840 850

60 70 80 90 100 110 120  
GGATTTTCATCAGACACTTC--CCTGGTATATCATGTACAGATTTATTAAGACACAGTATTAACAT  
|||||  
AGATTTATTTTCACTGCTCTCTTCCATTATTTCCAGAGACACACAGAGCCGCTAGAAAAAGACT  
860 870 880 890 900 910 920

130 140 150 160 170 180  
TTTTGACAGCT-----GCCGACACAAACTGCGAGTGGTTATTTCTTGAAGCGTGGTGC  
|||||  
TCCAGACACTTACATATATATATCATATGACACTGTTTAAAGGGGTCAACTATATGAAAACTATGTAATA  
930 940 950 960 970 980 990

190 200 210 220 230 240 250  
CCTGCAAAAGAGATGTTTCCGTTTCCATGAGCTGCTGAACCTTGCAGATCAAAACATATCCACATTC  
|||||  
AACAGATTTGGATGACAGACTCAGACATTAAGAAAGCAAAACAAAGAGATGGCTATTTCTGAAATTTAG  
1000 1010 1020 1030 1040 1050 1060

260 270 280 290 300 310 320  
AGATGTTCAAGAAAGCCAGACAGTACCTATTCGAAATCAAGATTAATTTGCTGTATATAGATG  
|||||  
TCATG-----ACATTCCTCATGATGATCAGATGCTC--ATACAGATTTATGCTTTCCAAATTTGACTT  
1070 1080 1090 1100 1110 1120

330 340 350 360 370 380 390  
GATTCATGACCAACCTATTTTGTAGTTTGTGAGCGGATGCT--AAAAATTTGAAGCCCAAGCTCAAGAA  
|||||  
GTTTGATTTGCAAAACAAATTTTACGTTTGAAGCCAAAGATGTTGAATGATTTATATATATGATAT  
1130 1140 1150 1160 1170 1180 1190 1200

400 410 420 430 440 450 460  
TTTATGTAACTGATCTTCAAGCAAAATACCTTGTGACATTTGAAAAGCCAAAGCAAAAAAAAA----  
|||||  
TTTAAAGCTGGTATCTTATATGTGAGCTTACATTTGTAACATTTGTAATAATTAATGAATCAATCAATG  
1210 1220 1230 1240 1250 1260 1270

470 480  
-----AAAAAAAAAAAA  
|||||  
GTTTTTAAAAAAAAAAAA  
1280 1290 X

12. US-09-746-783-18 (1-481)  
US-09-149-633-15 Sequence 15, Application US/09149633

Initial Score = 57 Optimized Score = 175 Significance = 0.67  
Residue Identity = 39% Matches = 192 Mismatches = 286  
Gaps = 12 Conservative Substitutions = 0

X  
GATACGTATATAAATAGAGACAGCTACAGTATCCAACTAAACCAACAGAG  
|||||  
ACCTTTCGCTTTAGAGCTTAACCTGAGATTTGTGTGNAAGGTTCCAAAGATCATGTAATTAAGGAGAT  
340 350 X 360 370 380 390 400

60 70 80 90 100 110 120  
GGATTTTCATCAGACACTTCCCTGCTGTAATCATGTATACAGATTTTAAAGACAGCAATGAATTTAAACATT  
|||||  
TTTCAATTTTTCATTTGTTTCCATGAAATGCAAAACATCATTTTAAATTAATAAAAAAAAAAGTTTCTT  
410 420 430 440 450 460 470

130 140 150 160 170 180  
TTTGACAGCTGCGGACACAAACTGCGAGTGTTCATTT-----TTCTTCAAGAAACGGTGTGGCTG  
|||||  
TACAAACAAATATGCAAGAAATATGAGCTTATATTTCTAGTATGATCAAAAGATGATGAGCTG

480	490	500	510	520	530	540	550
190	200	210	220	230	240	250	
CAAAAGATGTTCTGTTTTCATGAGCTGGCTGAACCTGTCAATCAAAACAAATACCAATTTAGAT							
AAATTTACATAGTAATATTTCAATACCT--TAGAATTCCTCAACCAAGTGAATAGCAAGAAGACGAT							
560	570	580	590	600	610	620	
260	270	280	290	300	310	320	330
GTTTCAGAAAGCCAGAAAGTAAACCTTTATTCAGAAATCAAAAGATATATTTGCTGTATATGAAAGTGAT							
TCTTCCCGAGAACTTAGAATTCACCACTGTTCGGTATATATCACTCCCTCCTGAATCGTTGAGAGCTCT							
630	640	650	660	670	680	690	
340	350	360	370	380	390	400	
CATGAGCAACCTGATTTTGGACTTTTGTGGAGCCGATGCTATAAAAATTTGGAAGCCAGAGCTCAGATTAAT							
TTAATTTGATTTTGTCTTGTCTCCCAAGTTAATATATTTATTTGATATCAAGAGTCAGCGCAAAAG							
700	710	720	730	740	750	760	
410	420	430	440	450	460	470	
GTAACCTGATCTCCAGCGCAAAATACACTGTGAKATTTGAAAAAGCGCAAAAAAAAAAAAAAAAAAAAA							
GAAACTTTTATCTCTAGGGAAGAAACATTTAGAAAAATGATTCAGTGATCTATCTGAAATGCGGAA							
770	780	790	800	810	820	830	
480	490	500	510	520	530	540	550
AAAAA							
AAATTTAATGTTAAAAAAACCTAT							
840	850	860					

13. US-09-746-783-18 (1-481)  
US-09-096-287-17 Sequence 17, Application US/09096287

Initial Score	-	55	Optimized Score	-	158	Significance	-	0.62
Residue Identity	-	34%	Matches	-	170	Mismatches	-	311
Gaps	-	10	Conservative Substitutions	-			-	0

GCATTTATATCAGCACTTCCGTTGGTATATCATGTGTACAGATTTATTTAAAGACACGAATTTTAAAAATTTT	60	70	80	90	100	110	120
CACACCCCTTCCGTGCTCCCCCACCACCCCTATGACCTTTACCCCTGGCTGGCCCTCCACAGGCCACCAAG	130	140	150	160	170	180	
TTTGG--ACAGCTCCCGGACACAACTCGACAGTGGTTCAATTTCTTGG-----AAAGCGTGTGTCCCTT	190	200	210	220	230	240	250
TTGGCTCTGTAGACCCCTCCCGCGCTGTGTATCAGCTCATCTTGTGCTGGGGGTAGAGATGAGGGAGGGAGTAA	260	270	280	290	300	310	320
GCAAAAGCATGTTTCTGTTTCCATGTAGACTGCTGAAACTGTGCATCTCAATAACAAATACCCACATTTTTCAGA	330	340	350	360	370	380	390
GTTAAACCTTGGACATAGCAAGATAGAAAGCTGGGGGAGATGCGTGCCTCAGTTTCTCCTCCACAACTGAAT	400	410	420	430	440	450	460
TTGTTTCAAGAAAAACCCAGAAAGTAAACCTTATTTCTCAAGATCAAAAAGAAATTAATTTGCTGTATTAGAAAGTGAAT	470	480	490	500	510	520	530
ATAGTGGCTGAAAACCTGGGGAGATACCTTGAATGAGCGCGGAATGCTGTTTCTCTCCCTCCACACCTCTTGAGAG	540	550	560	570	580	590	600
TCATATGCAACACTGATTTTGTGAGTTTGTGAGCCCGATCTTAAAAAATTTGAGGCCAAGCACTCAAGAATTTAA	610	620	630	640	650	660	670

[illegible]

14. US-09-746-783-18 (1-481)  
US-08-958-304-17 Sequence 17, Application US/08958304

Initial Score	-	54	Optimized Score	=	173	Significance	=	0.60
Residue Identity	-	38%	Matches	=	190	Mismatches	=	291
Gaps	-	11	Conservative Substitutions				=	0

[illegible]

120 130 140 150 160 170 180  
 AAACATTTTTCGACCTGCCGACCAAACTGCGAGTGTCTCAATTTTCTTCG--AACGCTGGTGCTCCTT  
 11 11 11 11 11 11 11  
 TAATATTCATATTATTACTATTCGCGAAGATGACCTTTGGCAAAAGCCGACCTTTGGCAGCTCATTTTAAACC  
 570 580 590 600 610 620 630  
 AGGTTTTTCCCGCCCTTTGAAACATTTTGGCTATTCATGAGAGTTTGCAATATTTTAACTTGTTGATGACAACTTT  
 11 11 11 11 11 11 11  
 GGAATTTT-----CATCAGACATCTCCCTGGTGCATATGTCAGATTTATTTAAACAGCAATTAATTTT  
 60 70 80 90 100 110  
 120 130 140 150 160 170 180  
 AAACATTTTTCGACCTGCCGACCAAACTGCGAGTGTCTCAATTTTCTTCG--AACGCTGGTGCTCCTT  
 11 11 11 11 11 11 11  
 TAATATTCATATTATTACTATTCGCGAAGATGACCTTTGGCAAAAGCCGACCTTTGGCAGCTCATTTTAAACC  
 570 580 590 600 610 620 630  
 AGGTTTTTCCCGCCCTTTGAAACATTTTGGCTATTCATGAGAGTTTGCAATATTTTAACTTGTTGATGACAACTTT  
 11 11 11 11 11 11 11  
 GGAATTTT-----CATCAGACATCTCCCTGGTGCATATGTCAGATTTATTTAAACAGCAATTAATTTT  
 60 70 80 90 100 110

[illegible]

ATGTAAAGTCTTCCTCCAAAGCCAAATTCACCTTGTGACATTTGCAAGGCGCAAAAAAAAAAAAAAAAAAAAAA  
 410 420 430 440 450 460 470  
 TTATGTACCTTTTTCATAACTGGAAATTGCCAAATTAAGCATGGAGATCTAAATGRRAAAAAAAAAAAAAAAAAAAA  
 850 860 870 880 890 900 910 920  
 X  
 AAAAAAAAA  
 |||  
 AAAGCGCCAGGCTTGAATTCATC  
 930 940

15. US-09-746-783-18 (1-481)

	270	280	290	300	310	320	330
AAGAAACCCGAMAGGTACCCTTTTTCAGAAATCAAAATAATTGGTCTGTATAGACTGGATTCATC							
TATTAAGCATCGTAGAACAATCTTCATCTTGAGCAACCTTTACATGATGGGTATTAATTTCAATCCGCAT							





